

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gorman, Daniel M.  
Randall, Troy D.  
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(ii) TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED REAGENTS

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/911,423  
(B) FILING DATE: 14-AUG-1997  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/023,419  
(B) FILING DATE: 16-AUG-1996

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: DX0612K

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1073 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 68..751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGAGATCC ATTGTGCTGG AAAGGAACT CCTGAAATCA GCCGACAGAA GACTCAGGAG	60
AAGCACT ATG GGG GCA TGG GCC ATG CTG TAT GGA GTC TCG ATG CTC TGT	109
Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys	
1 5 10	
GTG CTG GAC CTA GGT CAG CCG AGT GTA GTT GAG GAG CCT GGC TGT GGC	157
Val Leu Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly	
15 20 25 30	
CCT GGC AAG GTT CAG AAC GGA AGT GGC AAC AAC ACT CGC TGC TGC AGC	205
Pro Gly Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser	
35 40 45	
CTG TAT GCT CCA GGC AAG GAG GAC TGT CCA AAA GAA AGG TGC ATA TGT	253
Leu Tyr Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys	
50 55 60	
GTC ACA CCT GAG TAC CAC TGT GGA GAC CCT CAG TGC AAG ATC TGC AAG	301
Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys	
65 70 75	
CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGG GAT ATT	349
His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile	
80 85 90	
GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA	397
Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala	
95 100 105 110	
GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA	445
Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly	
115 120 125	
TTT CTC ACC ATG TTC CCT GGG AAC AAG ACC CAC AAT GCT GTG TGC ATC	493
Phe Leu Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile	
130 135 140	
CCG GAG CCA CTG CCC ACT GAG CAA TAC GGC CAT TTG ACT GTC ATC TTC	541
Pro Glu Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe	
145 150 155	
CTG GTC ATG GCT GCA TGC ATT TTC CTA ACC ACA GTC CAG CTC GGC	589
Leu Val Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly	
160 165 170	
CTG CAC ATA TGG CAG CTG AGG AGG CAA CAC ATG TGT CCC CGA GAG ACC	637

Leu His Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr				
175	180	185	190	
CAG CCA TTC GCG GAG GTG CAG TTG TCA GCT GAG GAT GCT TGC AGC TTC				685
Gln Pro Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe				
195	200	205		
CAG TTC CCT GAG GAG GAA CGC GGG GAG CAG ACA GAA GAA AAG TGT CAT				733
Gln Phe Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His				
210	215	220		
CTG GGG GGT CGG TGG CCA TGAGGCCCTGG TCTTCCTCTG TGCCCCAAGC				781
Leu Gly Gly Arg Trp Pro				
225				
CAGACGCTAC AAGACTTGCC CAGCTATAACC CTTGGTGAGA GCAGGGCCA TGCTCTGCAC				841
CCTTCCCTGG GCCTGGCCCT GCTCCCTCA ACAGTGGCCGG AAGTGGGTGT ATGAGAGCGG				901
TGAGTTACGA TTGGGCCCTA TGGCTGCCTT TCTCATTTGA CAGCTCTGTT GGAGTAGGGT				961
CTTTGGGCC ACCAAGAGCA CCACGTTAG CACAAGATCT TGTACAAGAA TAAATACTTG				1021
TTTAGTAACC TGAAAAAAA AAAAAGG CGGGCCGGG AGGCCGAATT CC				1073

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 228 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu				
1	5	10	15	
Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly				
20	25	30		
Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr				
35	40	45		
Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr				
50	55	60		
Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr				
65	70	75	80	
Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile Val Phe				
85	90	95		
Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala Gly Arg				
100	105	110		

Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly Phe Leu  
 115 120 125  
 Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile Pro Glu  
 130 135 140  
 Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe Leu Val  
 145 150 155 160  
 Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly Leu His  
 165 170 175  
 Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr Gln Pro  
 180 185 190  
 Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe Gln Phe  
 195 200 205  
 Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His Leu Gly  
 210 215 220  
 Gly Arg Trp Pro  
 225

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1006 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GCA CAG CAC GGG GCG ATG GGC GCG TTT CCG .GCC CTG TGC GGC CTG Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu	48
1 5 10 15	
GGC CTG CTG TGC GCG CTC AGC CTG GGT CAG CGC CCC ACC GGG GGT CCC Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro	96
20 25 30	
GGG TGC GGC CCT GGG CGC CTC CTG CTT GGG ACG GGA ACG GAC GCG CGC Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg	144
35 40 45	
TGC TGC CGG GTT CAC ACG ACG CGC TGC TGC CGC GAT TAC CCG GGC GAG Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu	192
50 55 60	

GAG TGC TGT TCC GAG TGG GAC TGC ATG TGT GTC CAG CCT GAA TTC CAC Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His 65 70 75 80	240
TGC GGA GAC CCT TGC TGC ACG ACC TGC CGG CAC CAC CCT TGT CCC CCA Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro 85 90 95	288
GCG CAG GGG GTA CAG TCC CAG GGG AAA TTC AGT TTT GGC TTC CAG TGT Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys 100 105 110	336
ATC GAC TGT GCC TCG GGG ACC TTC TCC GGG GGC CAC GAA GGC CAC TGC Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys 115 120 125	384
AAA CCT TGG ACA GAC TGC ACC CAG TTC GGG TTT CTC ACT GTG TTC CCT Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro 130 135 140	432
GGG AAC AAG ACC CAC AAC GCT GTG TGC GTC CCA GGG TCC CCG CCG GCA Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala 145 150 155 160	480
GAG CCG CTT GGG TGG CTG ACC GTC GTC CTC CTG GCC GTG GCC GCC TGC Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys 165 170 175	528
GTC CTC CTC CTG ACC TCG GCC CAG CTT GGA CTG CAC ATC TGG CAG CTG Val Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu 180 185 190	576
AGG AGT CAG TGC ATG TGG CCC CGA GAG ACC CAG CTG CTG CTG GAG GTG Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val 195 200 205	624
CCG CCG TCG ACC GAA GAC GCC AGA AGC TGC CAG TTC CCC GAG GAA GAG Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu 210 215 220	672
CGG GGC GAG CGA TCG GCA GAG GAG AAG GGG CGG CTG GGA GAC CTG TGG Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp 225 230 235 240	720
GTG TGAGCCTGGC CGTCCTCCGG GGCCACCGAC CGCAGCCAGC CCCTCCCCAG Val	773
GAGCTCCCCA GGCCGCAGGG GCTCTGCGTT CTGCTCTGGG CCGGGCCCTG CTCCCTGGC	833
AGCAGAACGTG GGTGCAGGAA GGTGGCAGTG ACCAGCGCCC TGGACCATGC AGTTGGCGG	893
CCGCTCTAAA GGATCCAAGC TTACGTACGC GTGCATGCGA CGTCATAGCT CTTCTATAGT	953
GTCACCTAAA TTCAATTACAC TGGCCGTCGT TTTACAACGT CCTGACTGGG AAA	1006

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu  
1 5 10 15

Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro  
20 25 30

Gly Cys Gly Pro Gly Arg Leu Leu Gly Thr Gly Thr Asp Ala Arg  
35 40 45

Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu  
50 55 60

Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His  
65 70 75 80

Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro  
85 90 95

Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys  
100 105 110

Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys  
115 120 125

Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro  
130 135 140

Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala  
145 150 155 160

Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys  
165 170 175

Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu  
180 185 190

Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Glu Val  
195 200 205

Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu  
210 215 220

Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp  
225 230 235 240

Val

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCNCARC AYGGNGCNAT GGGNGCNTTY MGNGCNYTNT GYGGNYTNGC NYTNYTNTGY	60
GCNYTNWSNY TNNGNCARMG NCCNACNGGN GGNCCNGGNT GYGGNCCNGG NMGNYTNYTN	120
YTNGGNACNG GNACNGAYGC NMGNNTGYTGY MGNGTNCAYA CNACNMGNTG YTGYMGNGAY	180
TAYCCNGGNG ARGARTGYTG YWSNGARTGG GAYTGYATGT GYGTNCARCC NGARTTYCAY	240
TGYGGNGAYC CNTGYTGYAC NACNTGYMGN CAYCAYCCNT GYCCNCCNGG NCARGGNGTN	300
CARWSNCARG GNAARTTYWS NTTYGGNTTY CARTGYATHG AYTGYGCNWS NGGNACNTTY	360
WSNGGNGNC AYGARGGNCA YTGYAARCCN TGGACNGAYT GYACNCARTT YGGNTTYYTN	420
ACNGTNTTYC CNGGNAAYAA RACNCAYAAY GCNGTNTGYG TNCCNGGNWS NCCNCCNGCN	480
GARCCNYTNG GNTGGYTNAC NGTNGTNYTN YTNGCNGTNG CNGCNGTGYGT NYTNYTNYTN	540
ACNWSNGCNC ARYTNGGNYT NCAYATHTGG CARYTNMGNW SNCARTGYAT GTGGCCNMGN	600
GARACNCARY TNYTNYTNGA RGTNCCNCCN WSNACNGARG AYGCNMGNWS NTGYCARTTY	660
CCNGARGARG ARMNGGGNGA RMGNWSNGCN GARGARAARG GNMGNYTNGG NGAYYTNTGG	720
GTN	723

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Gly	Ala	Phe	Arg	Ala	Leu	Cys	Gly	Leu	Ala	Leu	Leu	Cys	Ala	Leu
1					5				10				15		

Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg  
20 25 30

Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr  
35 40 45

Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp  
50 55 60

Asp Cys Met Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys  
65 70 75 80

Thr Thr Cys Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser  
85 90 95

Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys Ile Asp Cys Ala Ser Gly  
100 105 110

Thr Phe Ser Gly Gly His Glu Gly His Cys Lys Pro Trp Thr Asp Cys  
115 120 125

Thr Gln Phe Gly Phe Leu Thr Val Phe Pro Gly Asn Lys Thr His Asn  
130 135 140

Ala Val Cys Val Pro Gly Ser Pro Pro Ala Glu Pro Leu Gly Trp Leu  
145 150 155 160

Thr Val Val Leu Leu Ala Val Ala Ala Cys Val Leu Leu Leu Thr Ser  
165 170 175

Ala Gln Leu Gly Leu His Ile Trp Gln Leu Arg Lys Thr Gln Leu Leu  
180 185 190

Leu Glu Val Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro  
195 200 205

Glu Glu Glu Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly  
210 215 220

Asp Leu Trp Val  
225

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 232 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Gly	Ala	Phe	Arg	Ala	Leu	Cys	Gly	Leu	Ala	Leu	Leu	Cys	Ala	Leu
1															15
Ser	Leu	Gly	Gln	Arg	Pro	Thr	Gly	Gly	Pro	Gly	Cys	Gly	Pro	Gly	Arg
															30
Leu	Leu	Leu	Gly	Thr	Gly	Thr	Asp	Ala	Arg	Cys	Cys	Arg	Val	His	Thr
															45
Thr	Arg	Cys	Cys	Arg	Asp	Tyr	Pro	Gly	Glu	Cys	Cys	Ser	Glu	Trp	
															50
Asp	Cys	Met	Cys	Val	Gln	Pro	Glu	Phe	His	Cys	Gly	Asp	Pro	Cys	Cys
															65
Thr	Thr	Cys	Arg	His	His	Pro	Cys	Pro	Pro	Gly	Gln	Gly	Val	Gln	Ser
															85
Gln	Gly	Lys	Ser	Trp	Arg	Cys	Leu	Trp	Glu	Ser	Thr	Gln	Ala	Arg	Gly
															100
Ser	Thr	Arg	Ala	Arg	Gly	Arg	Ala	Arg	Gly	His	Arg	Cys	Pro	Ala	Arg
															115
Thr	Cys	Gly	Val	Trp	Gly	Pro	Glu	Ser	Cys	Glu	Ala	Gly	Gln	Ala	Arg
															130
Pro	Cys	Ser	Gly	Thr	Thr	Gly	His	Glu	Ala	Leu	Gly	Val	Ser	Cys	Pro
															145
Cys	Phe	Leu	Ser	Leu	Gly	Phe	Ser	Ile	Gln	His	Glu	Gly	Cys	Glu	Asn
															165
Pro	Ala	Gly	Arg	Trp	Gly	Arg	Val	Pro	Gly	Ala	Val	Trp	Leu	Ser	Gly
															180
Pro	Gly	His	Pro	Ser	Cys	Leu	Ser	Ser	Pro	His	Thr	Glu	Arg	Ala	Cys
															195
Pro	Val	Pro	Pro	Gly	Val	Leu	Ser	Gly	Ala	Trp	Gly	Cys	Thr	Leu	Phe
															210
Trp	Lys	Glu	Gln	Leu	Lys	Ser	Ser								
															225
															230

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 311 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu  
1 5 10 15

Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg  
20 25 30

Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr  
35 40 45

Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp  
50 55 60

Asp Cys Met Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys  
65 70 75 80

Thr Thr Cys Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser  
85 90 95

Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys Ile Asp Cys Ala Ser Gly  
100 105 110

Thr Phe Ser Gly Gly His Glu Gly His Cys Lys Pro Trp Thr Asp Cys  
115 120 125

Thr Gln Phe Gly Phe Leu Thr Val Phe Pro Gly Asn Lys Thr His Asn  
130 135 140

Ala Val Cys Val Pro Gly Ser Pro Pro Ala Glu Pro Leu Gly Trp Leu  
145 150 155 160

Thr Val Val Leu Leu Ala Val Ala Ala Cys Val Leu Leu Leu Thr Ser  
165 170 175

Ala Gln Leu Gly Leu His Ile Trp Gln Leu Arg Ser Gln Cys Met Trp  
180 185 190

Pro Arg Gly Leu Ser Gln Pro Gly Ala Gly Arg Trp Glu His Gly Cys  
195 200 205

Leu Leu Thr Val Ala Pro Leu Gln Arg Pro Ser Cys Cys Trp Arg Cys  
210 215 220

Arg Arg Arg Pro Lys Thr Pro Glu Ala Ala Ser Ser Pro Arg Lys Ser  
225 230 235 240

Gly Ala Ser Asp Arg Gln Arg Arg Gly Gly Trp Glu Thr Cys Gly  
245 250 255

Cys Glu Pro Gly Arg Pro Pro Gly Pro Pro Thr Ala Ala Ser Pro Ser  
260 265 270

Pro Gly Ala Pro Gln Ala Ala Gly Ala Leu Arg Ser Ala Leu Gly Arg  
275 280 285

Ala Leu Leu Pro Trp Gln Gln Lys Trp Val Gln Glu Gly Gly Ser Asp  
290 295 300

Gln Arg Pro Gly Pro Cys Ser  
305 310

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